



SEQUENCE LISTING

#3
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AUG 06 2001
TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shuping Tong et al.
- (ii) TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 225 Franklin Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/683,262
 - (B) FILING DATE: 18-JUL-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clark, Paul T.
 - (B) REGISTRATION NUMBER: 30,162
 - (C) REFERENCE/DOCKET NUMBER: 00786/287002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 542-5070
 - (B) TELEFAX: (617) 542-8906
 - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGATCTAT GGGCAGAATC TTTCCAC

27

(2) INFORMATION FOR SEQ ID NO:2:

09313066-080001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAATTCAG CGCAGGGTCC CCAAT

25

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCAGATCTAT GATGGGGCAA CATCCAGC

28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGAATTCAG GTACCAGACA TTTTCTTCTT

30

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGAATTCTT ATTCTAACT CTTGTAA

27

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GARYTNTAYG TNATGGAGAT

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAYTCNGGYT CNCCNGCYTC RTG

23

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TKYTNAGYCA YGARTTYCAR G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTKGCNGART ANARNGTYTC

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAAACAGA CACTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:11:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAACTCGA GCTGGAAGCA GTGTTATGAA

30

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGTACCAT GGAGGCGGCG CGGTGCATCG AGC

33

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTCGAGAT ATTAACATTA GCAATGTTAC T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	Arg	Glu	Ala	Phe	Arg	Arg
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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Gly Val His Glu Ala Gly Glu Pro Glu Phe Lys
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

Gly Arg Ile Ala
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

Thr Leu Tyr Ser Ala Lys
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

Val Glu Glu Gly Lys Val Pro Val Leu Asn Thr Pro Asp
1 5 10

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(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Glu Leu Tyr Val Met Glu Ile Ser Asp Asn Pro Gly Val His Glu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."

GAXCTNTAYG TNATGGAXAT WAGYGAYAAY CCNGGNGTNC AYGAXGCNGG NGAXCCNGAX	60
TTYAAX	66

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."
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GAXTTXTAYG TNATGGAXAT WTCNGAYAAY CCNGGNGTNC AYGAXGCNGG NGAXCCNGAX	60
TTYAAX	66

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(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "X is A or G."

GAXYTNTAYG TNATGGAGAT CTCGGACAAC CCCGGYGTYC AYGAXGCNGG NGAXCCNGAX 60

TT 62

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGAGATCT CGGACAACCC CGGCGTCCAT GAAGCAGGTG AGCCAGAGTT CAAG 54

(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

Ser Leu Leu Ser His Glu Phe Gln Asp Glu Thr Asp Thr Glu Glu Glu
1 5 10 15

Thr Leu Tyr Ser Ala Lys
20

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "X at positions 18, 24, 30, 42, 45, 48, and 66 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGYCTNCTNA GYCAYGAXTT YCAXGAYGAX ACNGAYACNG AXGAXGAXAC NCTNTAYAGY 60
GCNAAX 66

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "X at positions 6, 9, 18, 24, 30, 42, 45, 48, 54, and 66 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCNTTXXTTX CNCAYGAXTT YCAXGAYGAX ACNGAYACNG AXGAXGAXAC NTTXTAYTCN 60
GCNAAX 66

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Z at position 2 is G or T, X at positions 14, 20, and 44 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TZYTNAGYCA YGAXTTYCAX GATGAAACAG AACTGAAGA AGAXACNYTN TAYTCNGCVA 60
A 61

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(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

TCCCTTTTGA GCCACGAATT CCAGGATGAA ACAGACACTG AAGAA

45

(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS
(B) LOCATION: 1..481

ATG	GGG	CAA	CAT	CCA	GCA	AAA	TCA	ATG	GAC	GTC	AGA	CGG	ATA	GAA	GGA	48
Met	Gly	Gln	His	Pro	Ala	Lys	Ser	Met	Asp	Val	Arg	Arg	Ile	Glu	Gly	
1				5					10					15		
GGA	GAA	ATA	CTG	TTA	AAC	CAA	CTT	GCC	GGA	AGG	ATG	ATC	CCA	AAA	GGG	96
Gly	Glu	Ile	Leu	Leu	Asn	Gln	Leu	Ala	Gly	Arg	Met	Ile	Pro	Lys	Gly	
			20					25					30			
ACT	TTG	ACA	TGG	TCA	GGC	AAG	TTT	CCA	ACA	CTA	GAT	CAC	GTG	TTA	GAC	144
Thr	Leu	Thr	Trp	Ser	Gly	Lys	Phe	Pro	Thr	Leu	Asp	His	Val	Leu	Asp	
		35					40					45				
CAT	GTG	CAA	ACA	ATG	GAG	GAG	ATA	AAC	ACC	CTC	CAG	AAT	CAG	GGA	GCT	192
His	Val	Gln	Thr	Met	Glu	Glu	Ile	Asn	Thr	Leu	Gln	Asn	Gln	Gly	Ala	
	50					55					60					
TGG	CCT	GCT	GGG	GCG	GGA	AGG	AGA	GTA	GGA	TTA	TCA	AAT	CCG	ACT	CCT	240
Trp	Pro	Ala	Gly	Ala	Gly	Arg	Arg	Val	Gly	Leu	Ser	Asn	Pro	Thr	Pro	
65				70					75					80		
CAA	GAG	ATT	CCT	CAG	CCC	CAG	TGG	ACT	CCC	GAG	GAA	GAC	CAA	AAA	GCA	288
Gln	Glu	Ile	Pro	Gln	Pro	Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	
				85					90					95		
CGC	GAA	GCT	TTT	CGC	CGT	TAT	CAA	GAA	GAA	AGA	CCA	CCG	GAA	ACC	ACC	336
Arg	Glu	Ala	Phe	Arg	Arg	Tyr	Gln	Glu	Glu	Arg	Pro	Pro	Glu	Thr	Thr	
			100					105					110			

ACC ATT CCT CCG TCT TCC CCT CCT CAG TGG AAG CTA CAA CCC GGG GAC 384
 Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
 115 120 125

GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT CAT CCG CTA TAC 432
 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
 130 135 140

CAG TCA GAA CCA GCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG 481
 Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
 145 150 155 160

AAA 483
 Lys

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly
 1 5 10 15

Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
 20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
 35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
 50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
 65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
 85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
 100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
 115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
 130 135 140

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Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
 145 150 155 160

Lys

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Val	35	40	45	
Lys	Asp	Asp	Trp	Pro	Ala	Ala	Asn	Gln	Val	Gly	Val	Gly	Ala	Phe	Gly	50	55	60	
Pro	Arg	Leu	Thr	Pro	Pro	His	Gly	Gly	Ile	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Ser	Thr	Ile	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Ala	Phe	His	115	120	125	
Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Leu	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Ala	Pro	Asn	Ile	Ala	Ser	His	145	150	155	160
Ile	Ser	Ser	Ile	Ser	Ala	Arg	Thr	Gly	Asp	Pro	Val	Thr	Asn			165	170		

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Leu	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Thr	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Ile	35	40	45	
Lys	Asp	His	Trp	Pro	Ala	Ala	Asn	Gln	Val	Gly	Val	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Leu	Thr	Pro	Pro	His	Gly	Gly	Ile	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Ser	Thr	Ile	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Ala	Leu	His	115	120	125	
Gln	Ala	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Leu	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Ala	Pro	Asn	Ile	Ala	Ser	His	145	150	155	160
Ile	Ser	Ser	Ile	Ser	Ala	Arg	Thr	Gly	Asp	Pro	Val	Thr	Ile			165	170		

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu

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1	5	10	15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Ile	35	40	45
Lys Asp His Trp Pro Gln Ala Asn Gln Val Gly Val Gly Ala Phe Gly	50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Val Leu Gly Trp Ser Pro Gln	65	70	75
Ala Gln Gly Ile Leu Ala Thr Val Pro Ala Met Pro Pro Pro Ala Ser	85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu	100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Ala Phe His	115	120	125
Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly	130	135	140
Gly Ser Ser Ser Gly Thr Leu Asn Pro Val Pro Thr Ile Ala Ser His	145	150	155
Ile Ser Ser Ile Ser Ser Arg Ile Gly Asp Pro Ala Pro Asn	165	170	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu	1	5	10	15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30	
Ala Phe Lys Ala Asn Ser Asp Asn Pro Asp Trp Asp Leu Asn Pro His	35	40	45	
Lys Asp Asn Trp Pro Asp Ser Asn Lys Val Gly Val Gly Ala Phe Gly				

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50		55		60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		75 80
Ala Gln Gly Ile Leu Thr Thr Val Pro Thr Ala Pro Pro Pro Ala Ser				
	85		90	95
Thr Asn Arg Gln Leu Gly Arg Lys Pro Thr Pro Leu Ser Pro Pro Leu				
	100		105	110
Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His				
	115		120	125
Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly				
	130		135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Gln Asn Thr Val Ser Ser				
145		150		155 160
Ile Ser Ser Ile Leu Ser Lys Thr Gly Asp Pro Val Pro Asn				
	165		170	

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu				
1		5		10 15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro				
	20		25	30
Ala Phe Lys Ala Asn Ser Asp Asn Pro Asp Trp Asp Leu Asn Pro His				
	35		40	45
Lys Asp Asn Trp Pro Asp Ser Asn Lys Val Gly Val Gly Ala Phe Gly				
	50		55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		75 80
Ala Gln Gly Ile Leu Thr Thr Val Pro Thr Ala Pro Pro Pro Ala Ser				
	85		90	95
Thr Asn Arg Gln Leu Gly Arg Lys Pro Thr Pro Leu Ser Pro Pro Leu				

100	105	110
Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Thr Leu Gln Asp Pro Arg Val Arg Ala Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Gln Asn Thr Ala Ser Ser		
145	150	155
		160
Ile Ser Ser Ile Leu Ser Thr Thr Gly Asp Pro Val Pro Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu		
1	5	10
		15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro		
20	25	30
Ala Phe Lys Ala Asn Ser Glu Asn Pro Asp Trp Asp Leu Asn Pro Asn		
35	40	45
Lys Asp Asn Trp Pro Asp Ala Asn Lys Val Gly Val Gly Ala Phe Gly		
50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln		
65	70	75
		80
Ala Gln Gly Leu Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser		
85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu		
100	105	110
Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Thr Leu Gln Asp Pro Gly Val Arg Ala Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Ser Pro Ala Gln Asn Thr Val Ser Ala		

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1           5           10           15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20           25           30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
          35           40           45

Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly
          50           55           60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65           70           75           80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
          85           90           95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
          100          105          110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
          115          120          125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
          130          135          140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
145          150          155          160

Ile Ser Ser Thr Glu Ser Arg Thr Gly Asp Pro Ala Pro Asn
          165          170

```

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu

```

F02020-93081350

50		55		60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		80
Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu				
	100		105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His				
	115		120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly				
	130		135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro				
145		150		155
				160
Ile Ser Ser Ile Ser Phe Ser Thr Gly Asp Pro Ala Pro Asn				
	165		170	

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu				
1		5		10
				15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro				
	20		25	30
Ala Phe Gly Ala Asn Ser His Asn Pro Asp Trp Asp Phe Asn Pro Asn				
	35		40	45
Lys His Asp Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly				
	50		55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		75
				80
Ala Gln Gly Val Leu Thr Thr Val Pro Val Ala Pro Pro Pro Ala Ser				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu				

100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro		
145	150	155
Ile Ser Ser Ile Ser Ser Arg Thr Gly Asp Pro Ala Pro Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu		
1	5	10
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro		
20	25	30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn		
35	40	45
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly		
50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln		
65	70	75
Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser		
85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu		
100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro		

00018066.030201

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Gln	Gly	Met	Gly	Thr	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Ala	Phe	Gly	Ala	Asn	Ser	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn	35	40	45	
Lys	Asp	His	Trp	Pro	Glu	Ala	Asn	Gln	Val	Gly	Ala	Gly	Ala	Phe	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Ile	Leu	Thr	Thr	Val	Pro	Val	Ala	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Ile	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His	115	120	125	
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro	145	150	155	160
Ile	Ser	Ser	Ile	Phe	Ser	Arg	Thr	Gly	Asp	Pro	Ala	Pro	Asn			165	170		

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu

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1	5	10	15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn	35	40	45
Lys Asp His Trp Pro Ala Glu Asn Gln Val Gly Ala Gly Ala Phe Gly	50	55	60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln	65	70	75
Ala Gln Gly Ile Leu Thr Thr Leu Pro Ala Ala Pro Pro Pro Ala Ser	85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu	100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His	115	120	125
Gln Ala Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser	130	135	140
Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile	145	150	155
Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn	165	170	

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu	1	5	10	15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	20	25	30	
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn	35	40	45	
Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly				

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50		55		60
Pro Gly Phe Thr Pro Pro His Gly Leu Ile Leu Gly Trp Ser Pro Gln				
65		70		75
				80
Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Ser Ala Ser				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu				
	100		105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe Gln				
	115		120	125
Gln Ala Leu Gln Asp Pro Arg Val Arg Val Leu Tyr Phe Pro Ala Gly				
	130		135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu				
145		150		155
				160
Ile Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Val Thr Asn				
	165		170	

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu				
1		5		10
				15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro				
	20		25	30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn				
	35		40	45
Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly				
50		55		60
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		75
				80
Ala Gln Gly Ile Leu Thr Thr Leu Pro Ala Ala Pro Pro Pro Ala Ser				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu				

100	105	110
Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe Gln		
115	120	125
Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu		
145	150	155
		160
Ile Ser Ser Ile Ser Phe Ser Thr Gly Asp Pro Val Thr Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu		
1	5	10
		15
Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro		
20	25	30
Ala Phe Arg Ala Asn Thr Ala Asn Pro Asp Trp Asp Phe Asn Pro Asn		
35	40	45
Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly		
50	55	60
Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln		
65	70	75
		80
Ala Gln Gly Ile Leu Glu Leu Pro Ala Asn Ile Pro Pro Pro Ala Ser		
85	90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu		
100	105	110
Arg Asn Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Ala Phe His		
115	120	125
Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Leu Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Ala Pro Asn Ile Ala Ser His		

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

INFORMATION FOR SEQ ID NO:55:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu

1		5		10		15												
Ser	Thr	Ser	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro			
			20					25					30					
Ala	Phe	Arg	Ala	Asn	Thr	Asn	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn			
		35					40					45						
Lys	Asp	Thr	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly	Ala	Gly	Ala	Phe	Gly			
	50					55					60							
Leu	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln			
65					70					75					80			
Ala	Gln	Gly	Ile	Ile	Gln	Thr	Leu	Pro	Ala	Asn	Pro	Pro	Pro	Ala	Ser			
				85					90					95				
Thr	Asn	Arg	Gln	Ser	Gly	Arg	Gln	Pro	Thr	Pro	Leu	Ser	Pro	Pro	Leu			
			100					105					110					
Arg	Thr	Thr	His	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	His			
		115					120					125						
Gln	Thr	Leu	Gln	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	Gly			
	130					135					140							
Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	Pro			
145					150					155					160			
Ile	Ser	Ser	Ile	Phe	Ser	Arg	Ile	Gly	Asp	Pro	Ala	Leu	Asn					
			165					170										

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Gln	Asn	Leu		
1				5					10				15				
Ser	Thr	Ser	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro		
			20					25					30				
Ala	Phe	Arg	Ala	Asn	Thr	Ala	Asn	Pro	Asp	Trp	Asp	Phe	Asn	Pro	Asn		
		35					40					45					
Lys	Asp	Thr	Trp	Pro	Asp	Ala	Asn	Lys	Val	Gly	Ala	Gly	Ala	Phe	Gly		

102030" 99081860

50		55		60
Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
65		70		75 80
Ala Gln Gly Ile Leu Gln Thr Val Pro Ala Asn Pro Pro Pro Ala Ser				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu				
	100		105	110
Arg Asp Ala His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His				
	115		120	125
Gln Thr Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly				
	130		135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Leu Thr Thr Ala Ser Pro				
	145		150	155 160
Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Leu Ala Pro Asn				
	165		170	

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Gln Asn Leu				
1		5		10 15
Ser Thr Ser Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro				
	20		25	30
Ala Phe Arg Ala Asn Thr Arg Asn Pro Asp Trp Asp Phe Asn Pro Asn				
	35		40	45
Lys Asp Thr Trp Pro Asp Ala Asn Lys Val Gly Ala Gly Ala Phe Gly				
	50		55	60
Leu Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln				
	65		70	75 80
Ala Gln Gly Ile Leu Gln Thr Leu Pro Ala Asn Pro Pro Pro Ala Ala				
	85		90	95
Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu				

100	105	110
Arg Asp Ala His Pro Gln Ala Met Gln Trp Thr Ser Thr Thr Phe His		
115	120	125
Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly		
130	135	140
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro		
145	150	155 160
Ile Leu Ser Ile Phe Ser Lys Ile Gly Asp Leu Ala Pro Asn		
165	170	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Leu Ser Trp Thr Val Pro Leu Glu Gly Trp Gly Lys Asn His	
1 5 10 15	
Ser Thr Thr Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro	
20 25 30	
Ala Phe Arg Ala Asn Thr Arg Asn Pro Asp Trp Asp His Asn Pro Asn	
35 40 45	
Lys Asp His Trp Thr Glu Ala Asn Lys Val Gly Val Gly Ala Phe Gly	
50 55 60	
Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln	
65 70 75 80	
Ala Gln Gly Ile Met Lys Thr Leu Pro Ala Asp Pro Pro Pro Ala Ser	
85 90 95	
Thr Asn Arg Gln Ser Gly Arg Gln Pro Ile Pro Ile Thr Pro Pro Leu	
100 105 110	
Arg Asp Ser Thr Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His	
115 120 125	
Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Leu Phe Ala Gly	
130 135 140	
Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Leu	

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met	Gly	Ala	Pro	Leu	Ser	Thr	Thr	Arg	Arg	Gly	Met	Gly	Gln	Asn	Leu	1	5	10	15
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro	20	25	30	
Leu	Phe	Arg	Ala	Asn	Ser	Ser	Ser	Pro	Asp	Trp	Asp	Phe	Asn	Lys	Asn	35	40	45	
Lys	Asp	Thr	Trp	Pro	Met	Ala	Asn	Lys	Val	Gly	Val	Gly	Gly	Tyr	Gly	50	55	60	
Pro	Gly	Phe	Thr	Pro	Pro	His	Gly	Gly	Leu	Leu	Gly	Trp	Ser	Pro	Gln	65	70	75	80
Ala	Gln	Gly	Val	Leu	Thr	Thr	Leu	Pro	Ala	Asp	Pro	Pro	Pro	Ala	Ser	85	90	95	
Thr	Asn	Arg	Leu	Ser	Gly	Arg	Lys	Pro	Thr	Pro	Val	Ser	Pro	Pro	Leu	100	105	110	
Arg	Asp	Ser	Thr	Pro	Gln	Ala	Met	Gln	Trp	Asn	Ser	Thr	His	Phe	His	115	120	125	
Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Ala	Leu	Tyr	Phe	Pro	Ala	Gly	130	135	140	
Gly	Ser	Ser	Ser	Gly	Thr	Gln	Asn	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Leu	145	150	155	160
Thr	Ser	Ser	Ile	Ser	Ser	Lys	Thr	Gly	Gly	Pro	Ala	Met	Asn			165	170		

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Gly Ala Pro Leu Ser Thr Thr Arg Arg Gly Met Gly Thr Asn Leu

T02030-9908T260

50

55

60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Leu Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu
100 105 110

Arg Asp Thr His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Gln Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Leu Asn Pro Val Pro Asn Thr Ala Ser His
145 150 155 160

Ile Ser Ser Val Phe Ser Thr Thr Gly Asp Pro Ala Pro Asn
165 170

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT GAA GCA GGT GAG CCA GAG 48
Met Glu Ile Ser Asp Asn Pro Gly Val His Glu Ala Gly Glu Pro Glu
165 170 175

TTC AAG TAT ATT GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG CGA GAG 96
Phe Lys Tyr Ile Gly Asn Met His Gly Asn Glu Val Val Gly Arg Glu
180 185 190

CTG CTC CTG AAC CTC ATC GAG TAC CTC TGC AAG AAC TTC GGC ACA GAT 144
Leu Leu Leu Asn Leu Ile Glu Tyr Leu Cys Lys Asn Phe Gly Thr Asp
195 200 205

CCC GAA GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC CAC ATC ATG CCG 192
Pro Glu Val Thr Asp Leu Val Gln Ser Thr Arg Ile His Ile Met Pro
210 215 220

TCC ATG AAC CCA GAT GGC TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA 240

1020203-99021360

Ser	Met	Asn	Pro	Asp	Gly	Tyr	Glu	Lys	Ser	Gln	Glu	Gly	Asp	Arg	Gly	
225					230					235					240	
GGC	ACC	GTT	GGC	AGA	AAT	AAC	AGC	AAC	AAC	TAC	GAC	CTG	AAC	CGG	AAC	288
Gly	Thr	Val	Gly	Arg	Asn	Asn	Ser	Asn	Asn	Tyr	Asp	Leu	Asn	Arg	Asn	
				245					250					255		
TTC	CCA	GAT	CAG	TTC	TTC	CAG	GTG	ACA	GAC	CCT	CCG	CAG	CCA	GAA	ACT	336
Phe	Pro	Asp	Gln	Phe	Phe	Gln	Val	Thr	Asp	Pro	Pro	Gln	Pro	Glu	Thr	
			260					265					270			
CTT	GCT	GTC	ATG	AGC	TGG	TTG	AAA	ACT	TAC	CCG	TTC	GTG	CTT	TCA	GCA	384
Leu	Ala	Val	Met	Ser	Trp	Leu	Lys	Thr	Tyr	Pro	Phe	Val	Leu	Ser	Ala	
		275					280					285				
AAC	CTG	CAT	GGA	GGT	TCT	CTG	GTG	GTT	AAT	TAC	CCT	TTT	GAT	GAC	GAT	432
Asn	Leu	His	Gly	Gly	Ser	Leu	Val	Val	Asn	Tyr	Pro	Phe	Asp	Asp	Asp	
	290					295					300					
GAA	CAA	GGA	ATA	GCC	ATA	TAC	AGT	AAA	TCC	CCA	GAC	GAT	GCT	GTG	TTT	480
Glu	Gln	Gly	Ile	Ala	Ile	Tyr	Ser	Lys	Ser	Pro	Asp	Asp	Ala	Val	Phe	
305					310					315					320	
CAG	CAG	CTG	GCA	CTT	TCC	TAC	TCC	AAG	GAA	AAC	AAA	AAG	ATG	TAT	CAG	528
Gln	Gln	Leu	Ala	Leu	Ser	Tyr	Ser	Lys	Glu	Asn	Lys	Lys	Met	Tyr	Gln	
				325					330					335		
GGA	AGC	CCT	TGT	AAG	GAT	TTG	TAC	CCC	ACA	GAG	TAC	TTT	CCA	CAT	GGC	576
Gly	Ser	Pro	Cys	Lys	Asp	Leu	Tyr	Pro	Thr	Glu	Tyr	Phe	Pro	His	Gly	
			340					345					350			
ATC	ACG	AAC	GGG	GCC	CAG	TGG	TAC	AAC	GTT	CCA	GGT	GGG	ATG	CAG	GAC	624
Ile	Thr	Asn	Gly	Ala	Gln	Trp	Tyr	Asn	Val	Pro	Gly	Gly	Met	Gln	Asp	
		355					360					365				
TGG	AAT	TAC	TTA	AAT	ACC	AAC	CTG	TTT	GAA	GTG	ACC	ATT	GAG	CTG	GGC	672
Trp	Asn	Tyr	Leu	Asn	Thr	Asn	Leu	Phe	Glu	Val	Thr	Ile	Glu	Leu	Gly	
	370					375					380					
TGT	GTG	AAA	TAC	CCA	AAA	GCA	GAG	GAG	CTG	CCG	AAG	TAC	TGG	GAG	CAG	720
Cys	Val	Lys	Tyr	Pro	Lys	Ala	Glu	Glu	Leu	Pro	Lys	Tyr	Trp	Glu	Gln	
385					390					395					400	
AAC	CGT	AGA	TCT	CTC	CTC	CAG	TTC	ATT	AAA	CAG	GTT	CAC	CGC	GGC	ATC	768
Asn	Arg	Arg	Ser	Leu	Leu	Gln	Phe	Ile	Lys	Gln	Val	His	Arg	Gly	Ile	
				405					410					415		
TGG	GGA	TTT	GTG	CTG	GAT	GCC	ACG	GAC	GGA	AGG	GGC	ATT	CTC	AAC	GCC	816
Trp	Gly	Phe	Val	Leu	Asp	Ala	Thr	Asp	Gly	Arg	Gly	Ile	Leu	Asn	Ala	
			420					425					430			
ACC	ATC	AGC	GTC	GCC	GAC	ATC	AAC	CAC	CCC	GTG	ACC	ACC	TAC	AAA	GAT	864
Thr	Ile	Ser	Val	Ala	Asp	Ile	Asn	His	Pro	Val	Thr	Thr	Tyr	Lys	Asp	

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GGG GAC TAC TGG CGC CTC TTG GTC CAG GGG ACG TAC AAA GTC ACA GCA 912
Gly Asp Tyr Trp Arg Leu Leu Val Gln Gly Thr Tyr Lys Val Thr Ala
450 455 460

TCT GCC CGA GGG TAT GAT CCA GTC ACT AAA ACG GTG GAA GTC GAC AGC 960
Ser Ala Arg Gly Tyr Asp Pro Val Thr Lys Thr Val Glu Val Asp Ser
465 470 475 480

AAA GGT GGG GTG CAG GTC AAC TTC ACT CTT TCA CGG ACA GAC GCC AAA 1008
Lys Gly Gly Val Gln Val Asn Phe Thr Leu Ser Arg Thr Asp Ala Lys
485 490 495

GTG GAG GAG GGG AAG GTG CCA GTC CTG AAC ACC CCA GAC ACC AGC GAC 1056
Val Glu Glu Gly Lys Val Pro Val Leu Asn Thr Pro Asp Thr Ser Asp
500 505 510

CCC AAC GAG AAG GAG TTT GAG ACT CTG ATC AAA GAT CTA TCT GCT GAA 1104
Pro Asn Glu Lys Glu Phe Glu Thr Leu Ile Lys Asp Leu Ser Ala Glu
515 520 525

AAC GGC CTG GAG 1116
Asn Gly Leu
530

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Glu Ile Ser Asp Asn Pro Gly Val His Glu Ala Gly Glu Pro Glu
1 5 10 15

Phe Lys Tyr Ile Gly Asn Met His Gly Asn Glu Val Val Gly Arg Glu
20 25 30

Leu Leu Leu Asn Leu Ile Glu Tyr Leu Cys Lys Asn Phe Gly Thr Asp
35 40 45

Pro Glu Val Thr Asp Leu Val Gln Ser Thr Arg Ile His Ile Met Pro
50 55 60

Ser Met Asn Pro Asp Gly Tyr Glu Lys Ser Gln Glu Gly Asp Arg Gly
65 70 75 80

Gly Thr Val Gly Arg Asn Asn Ser Asn Asn Tyr Asp Leu Asn Arg Asn
85 90 95

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Phe	Pro	Asp	Gln	Phe	Phe	Gln	Val	Thr	Asp	Pro	Pro	Gln	Pro	Glu	Thr	100	105	110
Leu	Ala	Val	Met	Ser	Trp	Leu	Lys	Thr	Tyr	Pro	Phe	Val	Leu	Ser	Ala	115	120	125
Asn	Leu	His	Gly	Gly	Ser	Leu	Val	Val	Asn	Tyr	Pro	Phe	Asp	Asp	Asp	130	135	140
Glu	Gln	Gly	Ile	Ala	Ile	Tyr	Ser	Lys	Ser	Pro	Asp	Asp	Ala	Val	Phe	145	150	155
Gln	Gln	Leu	Ala	Leu	Ser	Tyr	Ser	Lys	Glu	Asn	Lys	Lys	Met	Tyr	Gln	165	170	175
Gly	Ser	Pro	Cys	Lys	Asp	Leu	Tyr	Pro	Thr	Glu	Tyr	Phe	Pro	His	Gly	180	185	190
Ile	Thr	Asn	Gly	Ala	Gln	Trp	Tyr	Asn	Val	Pro	Gly	Gly	Met	Gln	Asp	195	200	205
Trp	Asn	Tyr	Leu	Asn	Thr	Asn	Leu	Phe	Glu	Val	Thr	Ile	Glu	Leu	Gly	210	215	220
Cys	Val	Lys	Tyr	Pro	Lys	Ala	Glu	Glu	Leu	Pro	Lys	Tyr	Trp	Glu	Gln	225	230	235
Asn	Arg	Arg	Ser	Leu	Leu	Gln	Phe	Ile	Lys	Gln	Val	His	Arg	Gly	Ile	245	250	255
Trp	Gly	Phe	Val	Leu	Asp	Ala	Thr	Asp	Gly	Arg	Gly	Ile	Leu	Asn	Ala	260	265	270
Thr	Ile	Ser	Val	Ala	Asp	Ile	Asn	His	Pro	Val	Thr	Thr	Tyr	Lys	Asp	275	280	285
Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Val	Gln	Gly	Thr	Tyr	Lys	Val	Thr	Ala	290	295	300
Ser	Ala	Arg	Gly	Tyr	Asp	Pro	Val	Thr	Lys	Thr	Val	Glu	Val	Asp	Ser	305	310	315
Lys	Gly	Gly	Val	Gln	Val	Asn	Phe	Thr	Leu	Ser	Arg	Thr	Asp	Ala	Lys	325	330	335
Val	Glu	Glu	Gly	Lys	Val	Pro	Val	Leu	Asn	Thr	Pro	Asp	Thr	Ser	Asp	340	345	350
Pro	Asn	Glu	Lys	Glu	Phe	Glu	Thr	Leu	Ile	Lys	Asp	Leu	Ser	Ala	Glu	355	360	365
Asn	Gly	Leu	Glu													370		

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC	48
Phe Val Gln Asp Lys Ser Gly Lys Ala Ile Ser Lys Ala Thr Ile Val	
375 380 385	
CTT AAT GAA GGC TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT	96
Leu Asn Glu Gly Leu Arg Val Tyr Thr Lys Glu Gly Gly Tyr Phe His	
390 395 400	
GTG CTG TTG GCT CCT GGT TTG CAT AAC ATC AAT GCG ATA GCG GAT GGG	144
Val Leu Leu Ala Pro Gly Leu His Asn Ile Asn Ala Ile Ala Asp Gly	
405 410 415	
TAC CAA CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC GAT GCA CCC AGC	192
Tyr Gln Gln Lys His Met Lys Val Leu Val Arg His Asp Ala Pro Ser	
420 425 430 435	
TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT	240
Ser Val Phe Met Val Phe Asp Met Glu Asn Arg Ile Phe Gly Leu Pro	
440 445 450	
CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC	288
Arg Glu Leu Val Val Thr Val Ala Gly Ala Ile Met Ser Ala Leu Val	
455 460 465	
CTC ACT GCC TGT ATC ATC TGG TGT GTC TGC TCA ATC AAG GCC AAC AGA	336
Leu Thr Ala Cys Ile Ile Trp Cys Val Cys Ser Ile Lys Ala Asn Arg	
470 475 480	
CAC AAA GAT GGC TTC CAC TGC CGG CAG CAC CAC GAC GAT TAC GAG GAC	384
His Lys Asp Gly Phe His Cys Arg Gln His His Asp Asp Tyr Glu Asp	
485 490 495	
GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC CTT TTG AGC CAC	432
Glu Ile Arg Met Met Ser Thr Gly Ser Lys Lys Ser Leu Leu Ser His	
500 505 510 515	
GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA	462
Glu Phe Gln Asp Glu Thr Asp Thr Glu Glu	
520	

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(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Phe Val Gln Asp Lys Ser Gly Lys Ala Ile Ser Lys Ala Thr Ile Val
1 5 10 15
Leu Asn Glu Gly Leu Arg Val Tyr Thr Lys Glu Gly Gly Tyr Phe His
20 25 30
Val Leu Leu Ala Pro Gly Leu His Asn Ile Asn Ala Ile Ala Asp Gly
35 40 45
Tyr Gln Gln Lys His Met Lys Val Leu Val Arg His Asp Ala Pro Ser
50 55 60
Ser Val Phe Met Val Phe Asp Met Glu Asn Arg Ile Phe Gly Leu Pro
65 70 75 80
Arg Glu Leu Val Val Thr Val Ala Gly Ala Ile Met Ser Ala Leu Val
85 90 95
Leu Thr Ala Cys Ile Ile Trp Cys Val Cys Ser Ile Lys Ala Asn Arg
100 105 110
His Lys Asp Gly Phe His Cys Arg Gln His His Asp Asp Tyr Glu Asp
115 120 125
Glu Ile Arg Met Met Ser Thr Gly Ser Lys Lys Ser Leu Leu Ser His
130 135 140
Glu Phe Gln Asp Glu Thr Asp Thr Glu
145 150

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

His Gly Gly Ile Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr
 1 5 10 15
 Thr Val Ser Thr Ile Pro Pro Pro Ala Ser Thr Asn Arg Trp Ser Gly
 20 25 30
 Arg Trp Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His Pro Gln
 35 40 45

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro Gln Glu Ile Pro
 1 5 10 15
 Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala Arg Glu Ala Phe
 20 25 30
 Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr Thr Ile Pro Pro
 35 40 45

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Ala Arg Glu Ala Phe Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Val Ser Gly Val Leu Phe Gln Tyr Pro Asp Thr Glu Gly Lys
 1 5 10 15

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Glu Val Tyr Arg Leu Ala Leu Gln Thr Arg Glu Gln His Ile Arg Arg
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ser Gly Ala Gln Gly Glu Tyr Ala Gly Leu Ala Ala Ile Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Gln Pro Ile Glu Val Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2922 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAG GCG GCG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT GAC TTC	48
Glu Ala Ala Arg Cys Ile Glu Gln Leu Leu Pro Arg His Asp Asp Phe	
1 5 10 15	
TCC CGG CGG CAC ATC GGC CCC CGG GAG GGG GAG AAG AGG GAG ATG CTG	96
Ser Arg Arg His Ile Gly Pro Arg Glu Gly Glu Lys Arg Glu Met Leu	
20 25 30	
CGA GCC CTC GGG GTG CAG AGC GTC GAG GAG CTG ATG GAT AAA GCC ATC	144
Arg Ala Leu Gly Val Gln Ser Val Glu Glu Leu Met Asp Lys Ala Ile	
35 40 45	
CCG GGC AGC ATC CGG CTG CGC AGG CCG CTG AGG ATG GAG GAC CCC GTG	192
Pro Gly Ser Ile Arg Leu Arg Arg Pro Leu Arg Met Glu Asp Pro Val	
50 55 60	
GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT ATT GCA AGC AAG AAC	240
Gly Glu Asn Glu Ile Leu Glu Thr Leu Tyr Asn Ile Ala Ser Lys Asn	
65 70 75 80	
AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG	288
Lys Ile Trp Arg Ser Tyr Ile Gly Met Gly Tyr Tyr Asn Cys Ser Val	
85 90 95	
CCT CAA CCC ATT GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC	336
Pro Gln Pro Ile Ala Arg Asn Leu Leu Glu Asn Ala Gly Trp Val Thr	
100 105 110	
CAG TAT ACT CCC TAC CAA CCT GAG GTC TCA CAG GGC AGG CTG GAG AGC	384
Gln Tyr Thr Pro Tyr Gln Pro Glu Val Ser Gln Gly Arg Leu Glu Ser	
115 120 125	
CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA GGA ATG GAT GTG	432
Leu Leu Asn Tyr Gln Thr Met Val Cys Asp Ile Thr Gly Met Asp Val	
130 135 140	
GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG	480
Ala Asn Ala Ser Leu Leu Asp Glu Gly Thr Ala Ala Ala Glu Ala Met	
145 150 155 160	
CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC	528
Gln Leu Cys His Arg His Asn Lys Arg Arg Lys Phe Tyr Val Asp Ser	
165 170 175	
CGA TGC CAC CCT CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT	576
Arg Cys His Pro Gln Thr Ile Ala Val Val Gln Thr Arg Ala Asn Tyr	
180 185 190	
ACA GGT GTT ATT ACT GAG CTC AAA TTA CCC CAT GAG ATG GAT TTC AGT	624
Thr Gly Val Ile Thr Glu Leu Lys Leu Pro His Glu Met Asp Phe Ser	
195 200 205	
GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA GAC ACT GAG GGG	672
Gly Lys Asp Val Ser Gly Val Leu Phe Gln Tyr Pro Asp Thr Glu Gly	

210				215				220								
AAG	GTG	GAA	GAC	TTC	TCT	GAA	CTT	GTT	GAA	AGA	GCT	CAT	CAG	AAC	GGG	720
Lys	Val	Glu	Asp	Phe	Ser	Glu	Leu	Val	Glu	Arg	Ala	His	Gln	Asn	Gly	
225					230					235					240	
ACT	CTT	GCC	TGC	TGT	GCT	ACT	GAT	CTT	CTG	GCT	CTC	TGT	ATT	CTG	AAG	768
Thr	Leu	Ala	Cys	Cys	Ala	Thr	Asp	Leu	Leu	Ala	Leu	Cys	Ile	Leu	Lys	
				245					250					255		
CCT	CCT	GGA	GAG	TTT	GGG	GTA	GAT	GTT	GTC	CTG	GGT	AGC	TCC	CAG	AGA	816
Pro	Pro	Gly	Glu	Phe	Gly	Val	Asp	Val	Val	Leu	Gly	Ser	Ser	Gln	Arg	
			260					265					270			
TTT	GGT	GTG	CCA	CTC	TGC	TAT	GGG	GGA	CCC	CAC	GCA	GCA	TTC	TTC	GCT	864
Phe	Gly	Val	Pro	Leu	Cys	Tyr	Gly	Gly	Pro	His	Ala	Ala	Phe	Phe	Ala	
		275					280					285				
GTC	AAG	GAA	AAC	CTA	GTG	AGA	ATG	ATG	CCA	GGC	AGG	ATG	GTG	GGT	GTC	912
Val	Lys	Glu	Asn	Leu	Val	Arg	Met	Met	Pro	Gly	Arg	Met	Val	Gly	Val	
	290					295					300					
ACA	AGA	GAT	GCA	AAT	GGA	AAA	GAA	GTT	TAC	CGA	CTG	GCT	TTA	CAA	ACA	960
Thr	Arg	Asp	Ala	Asn	Gly	Lys	Glu	Val	Tyr	Arg	Leu	Ala	Leu	Gln	Thr	
305					310					315					320	
CGA	GAG	CAG	CAT	ATC	AGG	AGG	GAC	AAA	GCT	ACA	AGC	AAC	ATC	TGC	ACA	1008
Arg	Glu	Gln	His	Ile	Arg	Arg	Asp	Lys	Ala	Thr	Ser	Asn	Ile	Cys	Thr	
				325					330					335		
GCA	CAG	GCT	CTT	CTG	GCT	AAT	ATG	GCA	GCC	ATG	TTT	GGT	GTC	TAC	CAT	1056
Ala	Gln	Ala	Leu	Leu	Ala	Asn	Met	Ala	Ala	Met	Phe	Gly	Val	Tyr	His	
			340					345					350			
GGG	TCT	GAT	GGA	TTA	AGG	GAT	ATT	GCA	AGA	CGG	GTA	CAC	AAT	GCT	ACT	1104
Gly	Ser	Asp	Gly	Leu	Arg	Asp	Ile	Ala	Arg	Arg	Val	His	Asn	Ala	Thr	
		355					360					365				
TTA	ATC	CTG	GCT	GAA	GGT	CTC	AGG	AGA	GCT	GGT	CAT	AAA	CTG	CAC	CAT	1152
Leu	Ile	Leu	Ala	Glu	Gly	Leu	Arg	Arg	Ala	Gly	His	Lys	Leu	His	His	
	370					375					380					
GAT	CTG	TTC	TTT	GAT	ACC	TTG	ACA	GTC	ACG	TGT	GGA	TGC	TCA	GTC	AAA	1200
Asp	Leu	Phe	Phe	Asp	Thr	Leu	Thr	Val	Thr	Cys	Gly	Cys	Ser	Val	Lys	
385					390					395					400	
GAA	GTT	TTG	GAC	AGG	GCA	GCT	CTT	AGA	AAG	ATA	AAT	TTT	CGC	ATT	TAT	1248
Glu	Val	Leu	Asp	Arg	Ala	Ala	Leu	Arg	Lys	Ile	Asn	Phe	Arg	Ile	Tyr	
				405					410					415		
AGT	GAT	GGC	AGA	CTT	GGA	GTA	TCA	CTT	GAT	GAA	ACT	GTA	AGT	GAG	AAA	1296
Ser	Asp	Gly	Arg	Leu	Gly	Val	Ser	Leu	Asp	G						

GAC	CTA	GAT	GAC	ATA	TTA	TGG	ATT	TTT	GGT	TGC	GAG	TCT	TCA	GCT	GAA	1344	
Asp	Leu	Asp	Asp	Ile	Leu	Trp	Ile	Phe	Gly	Cys	Glu	Ser	Ser	Ala	Glu		
		435						440						445			
CTA	ATT	GCT	GAA	GGT	ATG	GGC	GAG	GAA	ACC	AAA	GGT	ATC	CTT	AGC	ACC	1392	
Leu	Ile	Ala	Glu	Gly	Met	Gly	Glu	Glu	Thr	Lys	Gly	Ile	Leu	Ser	Thr		
		450						455						460			
CCA	TTT	AAG	AGA	ACT	TCC	AAA	TTC	TTG	ACC	CAT	CAG	GTT	TTC	AAC	AGC	1440	
Pro	Phe	Lys	Arg	Thr	Ser	Lys	Phe	Leu	Thr	His	Gln	Val	Phe	Asn	Ser		
465					470						475			480			
TAT	CAC	TCC	GAA	ACA	AAT	ATC	GTA	CGG	TAC	ATG	AAG	AGA	TTA	GAA	AAC	1488	
Tyr	His	Ser	Glu	Thr	Asn	Ile	Val	Arg	Tyr	Met	Lys	Arg	Leu	Glu	Asn		
		485						490						495			
AAA	GAT	ATT	TCC	CTT	GTT	CAC	AGC	ATG	ATT	CCT	TTG	GGG	TCC	TGT	ACA	1536	
Lys	Asp	Ile	Ser	Leu	Val	His	Ser	Met	Ile	Pro	Leu	Gly	Ser	Cys	Thr		
		500						505						510			
ATG	AAG	CTC	AAT	AGT	TCA	GCT	GAA	CTT	GCA	CCT	ATT	TCA	TGG	AAG	GAA	1584	
Met	Lys	Leu	Asn	Ser	Ser	Ala	Glu	Leu	Ala	Pro	Ile	Ser	Trp	Lys	Glu		
		515						520						525			
TTT	GCC	AAC	ATC	CAC	CCC	TTT	GTG	CCC	TTG	GAT	CAA	GCT	CAA	GGG	TAT	1632	
Phe	Ala	Asn	Ile	His	Pro	Phe	Val	Pro	Leu	Asp	Gln	Ala	Gln	Gly	Tyr		
		530						535						540			
CAG	CAG	CTT	TTC	AAG	GAC	TTA	GAG	AAG	GAC	CTG	TGT	GAG	ATT	ACT	GGT	1680	
Gln	Gln	Leu	Phe	Lys	Asp	Leu	Glu	Lys	Asp	Leu	Cys	Glu	Ile	Thr	Gly		
545					550						555			560			
TAC	GAC	AAA	ATC	TCC	TTC	CAA	CCA	AAC	AGT	GGA	GCC	CAA	GGA	GAG	TAC	1728	
Tyr	Asp	Lys	Ile	Ser	Phe	Gln	Pro	Asn	Ser	Gly	Ala	Gln	Gly	Glu	Tyr		
		565						570						575			
GCA	GGC	TTG	GCC	GCA	ATC	AAA	GCT	TAT	TTA	AAT	GCA	AAA	GGA	GAA	CGT	1776	
Ala	Gly	Leu	Ala	Ala	Ile	Lys	Ala	Tyr	Leu	Asn	Ala	Lys	Gly	Glu	Arg		
		580						585						590			
CAT	CGA	AGT	GTT	TGC	CTT	ATT	CCT	AGA	TCT	GCT	CAT	GGT	ACA	AAT	CCA	1824	
His	Arg	Ser	Val	Cys	Leu	Ile	Pro	Arg	Ser	Ala	His	Gly	Thr	Asn	Pro		
		595						600						605			
GCA	AGT	GCA	CAG	ATG	GCA	GGG	ATG	AAG	ATT	CAA	CCA	GTT	GAA	GTA	GAT	1872	
Ala	Ser	Ala	Gln	Met	Ala	Gly	Met	Lys	Ile	Gln	Pro	Val	Glu	Val	Asp		
		610						615						620			
AAA	AAT	GGG	AGC	ATT	GAT	ATC	TCC	CAT	TTA	AAA	GCA	ATG	GTG	GAC	AAA	1920	
Lys	Asn	Gly	Ser	Ile	Asp	Ile	Ser	His	Leu	Lys	Ala	Met	Val	Asp	Lys		
625					630						635			640			
CAC	AAG	GAG	AAC	CTG	GCA	GCC	ATC	ATG	ATC	ACA	TAC	CCT	TCC	ACC	AAT	1968	
His	Lys	Glu	Asn	Leu	Ala	Ala	Ile	Met	Ile	Thr	Tyr	Pro	Ser	Thr	Asn		

			645					650					655						
GGT	GTG	TTT	GAG	GAG	GAG	ATT	GGG	GAT	GTG	TGT	GAG	CTG	ATT	CAC	AAA	2016			
Gly	Val	Phe	Glu	Glu	Glu	Ile	Gly	Asp	Val	Cys	Glu	Leu	Ile	His	Lys				
			660					665					670						
AAC	GGA	GGC	CAG	GTT	TAC	CTG	GAT	GGA	GCA	AAC	ATG	AAC	GCC	CAA	GTG	2064			
Asn	Gly	Gly	Gln	Val	Tyr	Leu	Asp	Gly	Ala	Asn	Met	Asn	Ala	Gln	Val				
			675					680					685						
GGT	CTG	TGT	CGT	CCT	GGA	GAT	TAT	GGC	TCT	GAT	GTC	TCT	CAC	TTA	AAC	2112			
Gly	Leu	Cys	Arg	Pro	Gly	Asp	Tyr	Gly	Ser	Asp	Val	Ser	His	Leu	Asn				
			690					695					700						
CTT	CAC	AAA	ACC	TTT	TGC	ATT	CCC	CAT	GGA	GGA	GGA	GGA	CCT	GGA	ATG	2160			
Leu	His	Lys	Thr	Phe	Cys	Ile	Pro	His	Gly	Gly	Gly	Gly	Pro	Gly	Met				
705			710					715					720						
GGA	CCA	ATT	GGA	GTG	AAG	AAA	CAT	CTG	GCT	CCC	TAC	TTG	CCT	ACC	CAT	2208			
Gly	Pro	Ile	Gly	Val	Lys	Lys	His	Leu	Ala	Pro	Tyr	Leu	Pro	Thr	His				
			725					730					735						
CCT	GTC	ATC	AAG	ATT	CAG	ACG	GAT	AAG	GAT	GCA	TGT	CCT	TTG	GGT	ACT	2256			
Pro	Val	Ile	Lys	Ile	Gln	Thr	Asp	Lys	Asp	Ala	Cys	Pro	Leu	Gly	Thr				
			740					745					750						
GTC	AGT	GCT	GCA	CCT	TGG	GGT	TCC	AGT	GCT	ATA	TTG	CCT	ATT	TCC	TGG	2304			
Val	Ser	Ala	Ala	Pro	Trp	Gly	Ser	Ser	Ala	Ile	Leu	Pro	Ile	Ser	Trp				
			755					760					765						
GTG	TAT	ATC	AAG	ACA	ATG	GGA	GCA	AAG	GGT	CTT	AAA	CAC	GCT	TCT	GAG	2352			
Val	Tyr	Ile	Lys	Thr	Met	Gly	Ala	Lys	Gly	Leu	Lys	His	Ala	Ser	Glu				
			770					775					780						
GTT	GCT	ATA	TTA	AAT	GCA	AAC	TAC	ATG	GCA	AAG	AGG	CTG	GAG	AAG	CAC	2400			
Val	Ala	Ile	Leu	Asn	Ala	Asn	Tyr	Met	Ala	Lys	Arg	Leu	Glu	Lys	His				
785			790					795					800						
TAC	AAA	ATC	CTT	TTC	AGA	GGA	GTA	AGA	GGT	TAT	GTA	GCC	CAT	GAA	TTC	2448			
Tyr	Lys	Ile	Leu	Phe	Arg	Gly	Val	Arg	Gly	Tyr	Val	Ala	His	Glu	Phe				
			805					810					815						
ATT	TTG	GAT	ACA	AGA	CCT	TTC	AAA	AAA	ACA	GCA	AAC	ATT	GAA	GCT	GTG	2496			
Ile	Leu	Asp	Thr	Arg	Pro	Phe	Lys	Lys	Thr	Ala	Asn	Ile	Glu	Ala	Val				
			820					825					830						
GAT	CTT	GCT	AAG	CGA	CTT	CAG	GAT	TAT	GGT	TTT	CAT	GCT	CCA	ACC	ATG	2544			
Asp	Leu	Ala	Lys	Arg	Leu	Gln	Asp	Tyr	Gly	Phe	His	Ala	Pro	Thr	Met				
			835					840					845						
TCC	TGG	CCA	GTG	GCA	GGC	ACA	CTT	ATG	ATT	GAA	CCA	ACA	GAG	TCT	GAA	2592			
Ser	Trp	Pro	Val	Ala	Gly	Thr	Leu	Met	Ile	Glu	Pro	Thr	Glu	Ser	Glu				
			850					855					860						

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Lys	Ile	Trp	Arg	Ser	Tyr	Ile	Gly	Met	Gly	Tyr	Tyr	Asn	Cys	Ser	Val	85	90	95	
Pro	Gln	Pro	Ile	Ala	Arg	Asn	Leu	Leu	Glu	Asn	Ala	Gly	Trp	Val	Thr	100	105	110	
Gln	Tyr	Thr	Pro	Tyr	Gln	Pro	Glu	Val	Ser	Gln	Gly	Arg	Leu	Glu	Ser	115	120	125	
Leu	Leu	Asn	Tyr	Gln	Thr	Met	Val	Cys	Asp	Ile	Thr	Gly	Met	Asp	Val	130	135	140	
Ala	Asn	Ala	Ser	Leu	Leu	Asp	Glu	Gly	Thr	Ala	Ala	Ala	Glu	Ala	Met	145	150	155	160
Gln	Leu	Cys	His	Arg	His	Asn	Lys	Arg	Arg	Lys	Phe	Tyr	Val	Asp	Ser	165	170	175	
Arg	Cys	His	Pro	Gln	Thr	Ile	Ala	Val	Val	Gln	Thr	Arg	Ala	Asn	Tyr	180	185	190	
Thr	Gly	Val	Ile	Thr	Glu	Leu	Lys	Leu	Pro	His	Glu	Met	Asp	Phe	Ser	195	200	205	
Gly	Lys	Asp	Val	Ser	Gly	Val	Leu	Phe	Gln	Tyr	Pro	Asp	Thr	Glu	Gly	210	215	220	
Lys	Val	Glu	Asp	Phe	Ser	Glu	Leu	Val	Glu	Arg	Ala	His	Gln	Asn	Gly	225	230	235	240
Thr	Leu	Ala	Cys	Cys	Ala	Thr	Asp	Leu	Leu	Ala	Leu	Cys	Ile	Leu	Lys	245	250	255	
Pro	Pro	Gly	Glu	Phe	Gly	Val	Asp	Val	Val	Leu	Gly	Ser	Ser	Gln	Arg	260	265	270	
Phe	Gly	Val	Pro	Leu	Cys	Tyr	Gly	Gly	Pro	His	Ala	Ala	Phe	Phe	Ala	275	280	285	
Val	Lys	Glu	Asn	Leu	Val	Arg	Met	Met	Pro	Gly	Arg	Met	Val	Gly	Val	290	295	300	
Thr	Arg	Asp	Ala	Asn	Gly	Lys	Glu	Val	Tyr	Arg	Leu	Ala	Leu	Gln	Thr	305	310	315	320
Arg	Glu	Gln	His	Ile	Arg	Arg	Asp	Lys	Ala	Thr	Ser	Asn	Ile	Cys	Thr	325	330	335	
Ala	Gln	Ala	Leu	Leu	Ala	Asn	Met	Ala	Ala	Met	Phe	Gly	Val	Tyr	His	340	345	350	
Gly	Ser	Asp	Gly	Leu	Arg	Asp	Ile	Ala	Arg	Arg	Val	His	Asn	Ala	Thr	355	360	365	

Leu	Ile	Leu	Ala	Glu	Gly	Leu	Arg	Arg	Ala	Gly	His	Lys	Leu	His	His	370	375	380	
Asp	Leu	Phe	Phe	Asp	Thr	Leu	Thr	Val	Thr	Cys	Gly	Cys	Ser	Val	Lys	385	390	395	400
Glu	Val	Leu	Asp	Arg	Ala	Ala	Leu	Arg	Lys	Ile	Asn	Phe	Arg	Ile	Tyr	405	410	415	
Ser	Asp	Gly	Arg	Leu	Gly	Val	Ser	Leu	Asp	Glu	Thr	Val	Ser	Glu	Lys	420	425	430	
Asp	Leu	Asp	Asp	Ile	Leu	Trp	Ile	Phe	Gly	Cys	Glu	Ser	Ser	Ala	Glu	435	440	445	
Leu	Ile	Ala	Glu	Gly	Met	Gly	Glu	Glu	Thr	Lys	Gly	Ile	Leu	Ser	Thr	450	455	460	
Pro	Phe	Lys	Arg	Thr	Ser	Lys	Phe	Leu	Thr	His	Gln	Val	Phe	Asn	Ser	465	470	475	480
Tyr	His	Ser	Glu	Thr	Asn	Ile	Val	Arg	Tyr	Met	Lys	Arg	Leu	Glu	Asn	485	490	495	
Lys	Asp	Ile	Ser	Leu	Val	His	Ser	Met	Ile	Pro	Leu	Gly	Ser	Cys	Thr	500	505	510	
Met	Lys	Leu	Asn	Ser	Ser	Ala	Glu	Leu	Ala	Pro	Ile	Ser	Trp	Lys	Glu	515	520	525	
Phe	Ala	Asn	Ile	His	Pro	Phe	Val	Pro	Leu	Asp	Gln	Ala	Gln	Gly	Tyr	530	535	540	
Gln	Gln	Leu	Phe	Lys	Asp	Leu	Glu	Lys	Asp	Leu	Cys	Glu	Ile	Thr	Gly	545	550	555	560
Tyr	Asp	Lys	Ile	Ser	Phe	Gln	Pro	Asn	Ser	Gly	Ala	Gln	Gly	Glu	Tyr	565	570	575	
Ala	Gly	Leu	Ala	Ala	Ile	Lys	Ala	Tyr	Leu	Asn	Ala	Lys	Gly	Glu	Arg	580	585	590	
His	Arg	Ser	Val	Cys	Leu	Ile	Pro	Arg	Ser	Ala	His	Gly	Thr	Asn	Pro	595	600	605	
Ala	Ser	Ala	Gln	Met	Ala	Gly	Met	Lys	Ile	Gln	Pro	Val	Glu	Val	Asp	610	615	620	
Lys	Asn	Gly	Ser	Ile	Asp	Ile	Ser	His	Leu	Lys	Ala	Met	Val	Asp	Lys	625	630	635	640
His	Lys	Glu	Asn	Leu	Ala	Ala	Ile	Met	Ile	Thr	Tyr	Pro	Ser	Thr	Asn	645	650	655	

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Gly	Val	Phe	Glu	Glu	Glu	Ile	Gly	Asp	Val	Cys	Glu	Leu	Ile	His	Lys	660	665	670	
Asn	Gly	Gly	Gln	Val	Tyr	Leu	Asp	Gly	Ala	Asn	Met	Asn	Ala	Gln	Val	675	680	685	
Gly	Leu	Cys	Arg	Pro	Gly	Asp	Tyr	Gly	Ser	Asp	Val	Ser	His	Leu	Asn	690	695	700	
Leu	His	Lys	Thr	Phe	Cys	Ile	Pro	His	Gly	Gly	Gly	Gly	Pro	Gly	Met	705	710	715	720
Gly	Pro	Ile	Gly	Val	Lys	Lys	His	Leu	Ala	Pro	Tyr	Leu	Pro	Thr	His	725	730	735	
Pro	Val	Ile	Lys	Ile	Gln	Thr	Asp	Lys	Asp	Ala	Cys	Pro	Leu	Gly	Thr	740	745	750	
Val	Ser	Ala	Ala	Pro	Trp	Gly	Ser	Ser	Ala	Ile	Leu	Pro	Ile	Ser	Trp	755	760	765	
Val	Tyr	Ile	Lys	Thr	Met	Gly	Ala	Lys	Gly	Leu	Lys	His	Ala	Ser	Glu	770	775	780	
Val	Ala	Ile	Leu	Asn	Ala	Asn	Tyr	Met	Ala	Lys	Arg	Leu	Glu	Lys	His	785	790	795	800
Tyr	Lys	Ile	Leu	Phe	Arg	Gly	Val	Arg	Gly	Tyr	Val	Ala	His	Glu	Phe	805	810	815	
Ile	Leu	Asp	Thr	Arg	Pro	Phe	Lys	Lys	Thr	Ala	Asn	Ile	Glu	Ala	Val	820	825	830	
Asp	Leu	Ala	Lys	Arg	Leu	Gln	Asp	Tyr	Gly	Phe	His	Ala	Pro	Thr	Met	835	840	845	
Ser	Trp	Pro	Val	Ala	Gly	Thr	Leu	Met	Ile	Glu	Pro	Thr	Glu	Ser	Glu	850	855	860	
Asp	Lys	Ala	Glu	Leu	Asp	Arg	Phe	Cys	Asp	Ala	Met	Ile	Ser	Ile	Arg	865	870	875	880
Gln	Glu	Ile	Ala	Glu	Ile	Glu	Glu	Gly	Arg	Met	Asp	Pro	Gln	Ile	Asn	885	890	895	
Pro	Leu	Lys	Met	Ser	Pro	His	Thr	Leu	Asn	Cys	Val	Thr	Ser	Ser	Lys	900	905	910	
Trp	Asp	Arg	Pro	Tyr	Ser	Arg	Glu	Val	Ala	Ala	Phe	Pro	Leu	Pro	Phe	915	920	925	
Val	Lys	Pro	Glu	Ser	Lys	Phe	Trp	Pro	Thr	Ile	Ala	Arg	Ile	Asp	Asp				

